

**STIC Biotechnology Systems Branch****RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/524,263  
Source: P4/10  
Date Processed by STIC: 2/23/05

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



PCT

*see item 4 on Error Summary Sheet*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/524,263

DATE: 02/23/2005

TIME: 09:14:13

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\02232005\J524263.raw

3 <110> APPLICANT: HITACHI HIGH-TECHNOLOGIES CORPORATION  
 5 <120> TITLE OF INVENTION: METHOD AND APPARATUS FOR DETECTING NUCLEIC ACID  
 7 <130> FILE REFERENCE: PH-1502-PCT  
 9 <140> CURRENT APPLICATION NUMBER: US/10/524,263  
 10 <141> CURRENT FILING DATE: 2005-02-11  
 12 <160> NUMBER OF SEQ ID NOS: 3  
 14 <170> SOFTWARE: PatentIn Ver. 2.1

*OK*

## ERRORED SEQUENCES

34 <210> SEQ ID NO: 3  
 35 <211> LENGTH: 50  
 36 <212> TYPE: DNA  
 37 <213> ORGANISM: Artificial Sequence  
 W--> 39 <220> FEATURE:  
 W--> 39 <223> OTHER INFORMATION:  
 W--> 39 <400> 3  
 C--> 40 tctagcctca atcctcatatc  
 E--> 46 1/2  
 E--> 47 dsmdb.1883558.1

*pp 1-2*  
**Does Not Comply**  
**Corrected Diskette Needed**

*see p. 2 for error explanation*

*20 (same error in sequences 1 and 2)*

*use lower-case letters for nucleotides*

*delete*

**BEST AVAILABLE COPY**

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/524,263

DATE: 02/23/2005  
TIME: 09:14:14

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\02232005\J524263.raw

*error explanation*

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:1,2,3

BEST AVAILABLE COPY

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/524,263

DATE: 02/23/2005

TIME: 09:14:14

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\02232005\J524263.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:21 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>  
ORGANISM:Artificial Sequence  
L:21 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>  
ORGANISM:Artificial Sequence  
L:21 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:21  
L:22 M:112 C: (48) String data converted to lower case,  
L:30 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>  
ORGANISM:Artificial Sequence  
L:30 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>  
ORGANISM:Artificial Sequence  
L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:30  
L:31 M:112 C: (48) String data converted to lower case,  
L:39 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:3, <213>  
ORGANISM:Artificial Sequence  
L:39 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>  
ORGANISM:Artificial Sequence  
L:39 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:39  
L:40 M:112 C: (48) String data converted to lower case,  
L:46 M:254 E: No. of Bases conflict, LENGTH:Input:2 Counted:21 SEQ:3  
L:46 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
M:254 Repeated in SeqNo=3  
L:47 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9  
M:112 Repeated in SeqNo=3  
L:47 M:252 E: No. of Seq. differs, <211> LENGTH:Input:50 Found:28 SEQ:3

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>10/524,263</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino <input type="checkbox"/> Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 <input type="checkbox"/> "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) <input type="checkbox"/> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 <input type="checkbox"/> "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	

AMC - Biotechnology Systems Branch - 09/09/2003

BEST AVAILABLE COPY